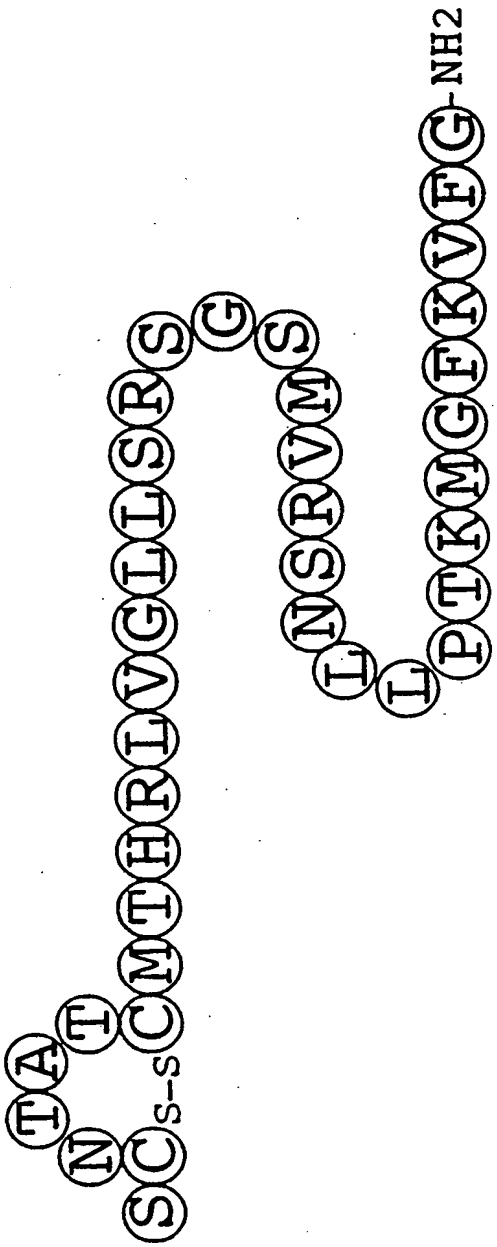
Fig. 1



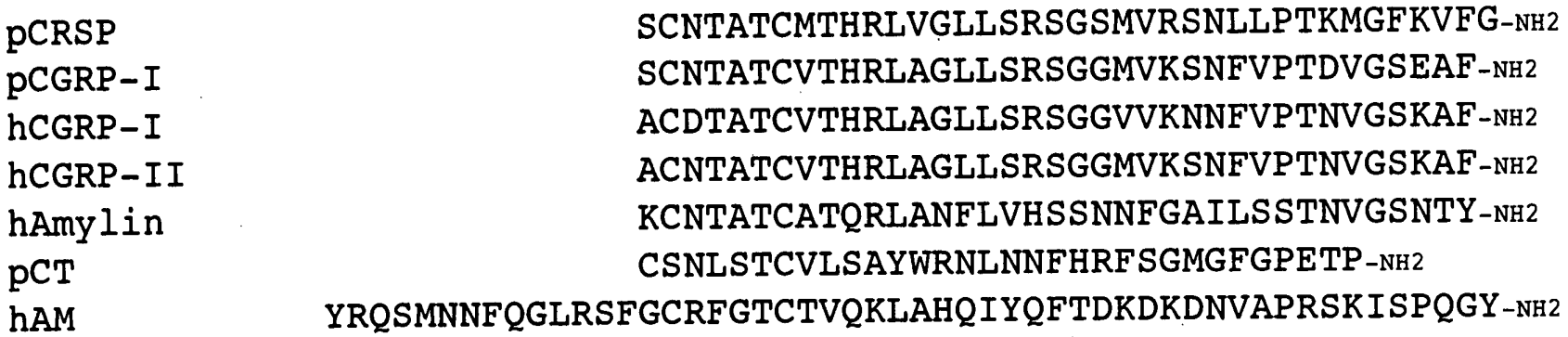

pCRSP SCNTATCMTHRLVGLLSRSGSMVRSNLLPTKMGFKVFG-NH2
pCGRP-I SCNTATCVTHRLAGLLSRSGGMVKSNFVPTDVGSEAF-NH2
hCGRP-I ACDTATCVTHRLAGLLSRSGGVVKNNFVPTNVGSKAF-NH2
hCGRP-II ACNTATCVTHRLAGLLSRSGGMVKSNFVPTNVGSKAF-NH2
hAmylin KCNTATCATQRLANFLVHSSNNFGAILSSTNVGSNTY-NH2
pCT CSNLSTCVLSAYWRNLNNFHRFSGMGFGPETP-NH2
hAM YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY-NH2

Fig. 2

Fig. 3

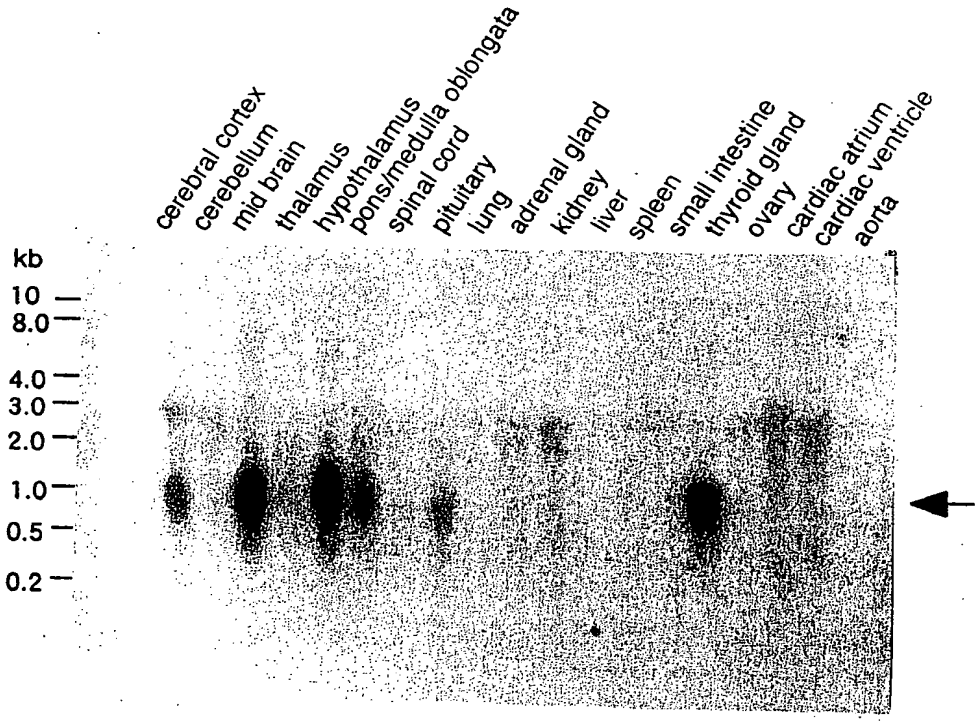

cerebral cortex
cerebellum
mid brain
thalamus
hypothalamus
pons/medulla oblongata
spinal cord
pituitary
lung
adrenal gland
kidney
liver
spleen
small intestine
thyroid gland
ovary
cardiac atrium
cardiac ventricle
aorta
kb
10
8.0
4.0
3.0
2.0
1.0
0.5
0.2

Fig. 4

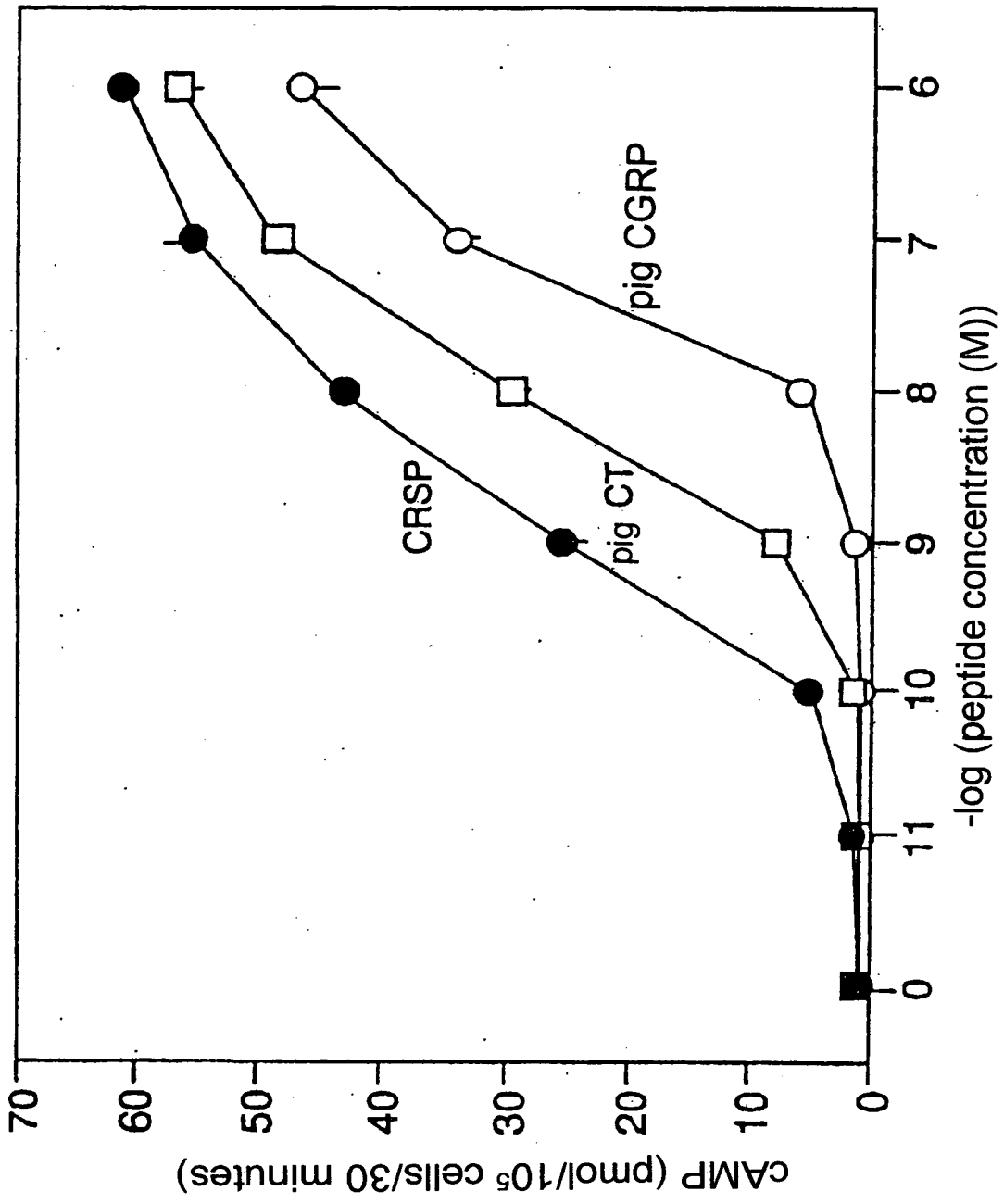

cAMP (pmol/10⁵ cells/30 minutes)
70
60
50
40
30
20
10
0
-log (peptide concentration (M))
0
11
10
9
8
7
6
CRSP
pig CT
pig CGRP

Fig. 5

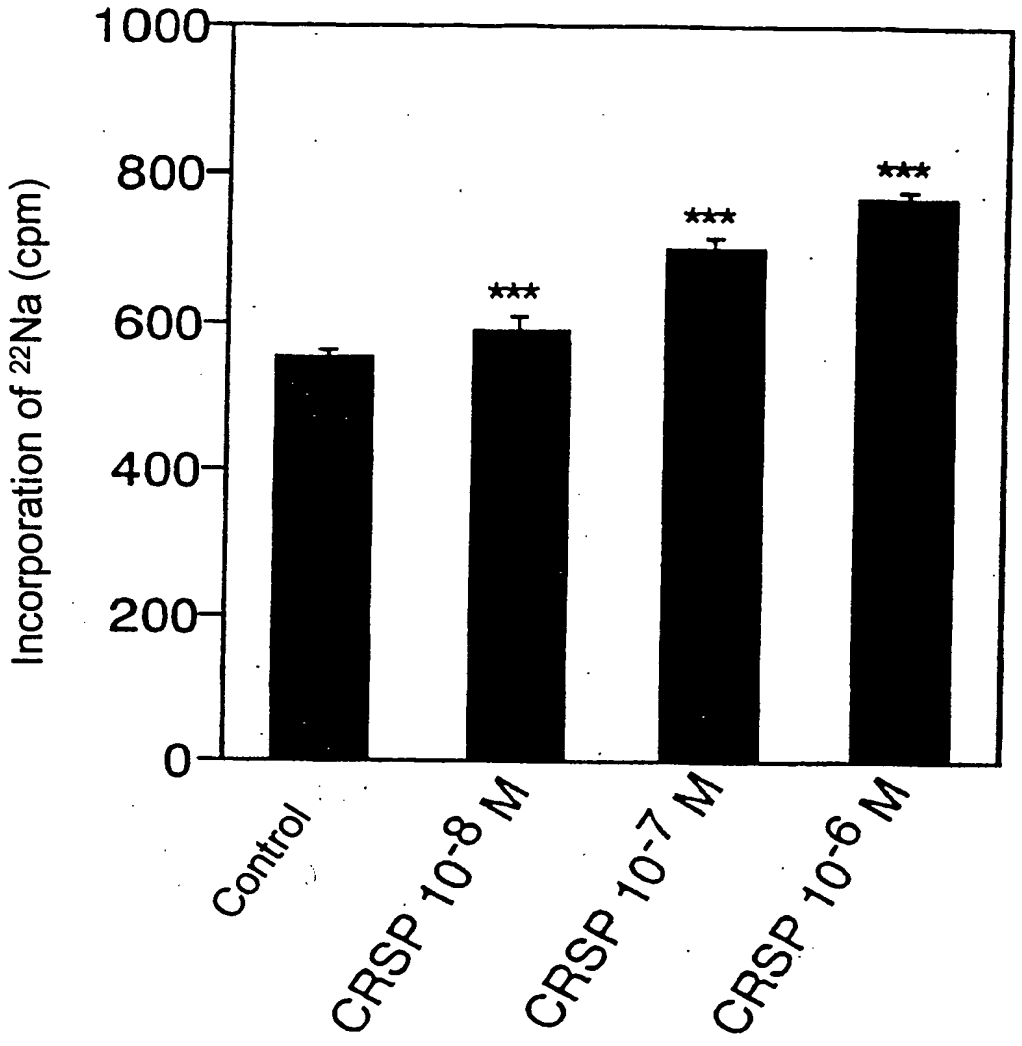

1000
800
600
400
200
0
Incorporation of ^{22}Na (cpm)
***
***
***
Control
CRSP 10-8 M
CRSP 10-7 M
CRSP 10-6 M

Fig. 6

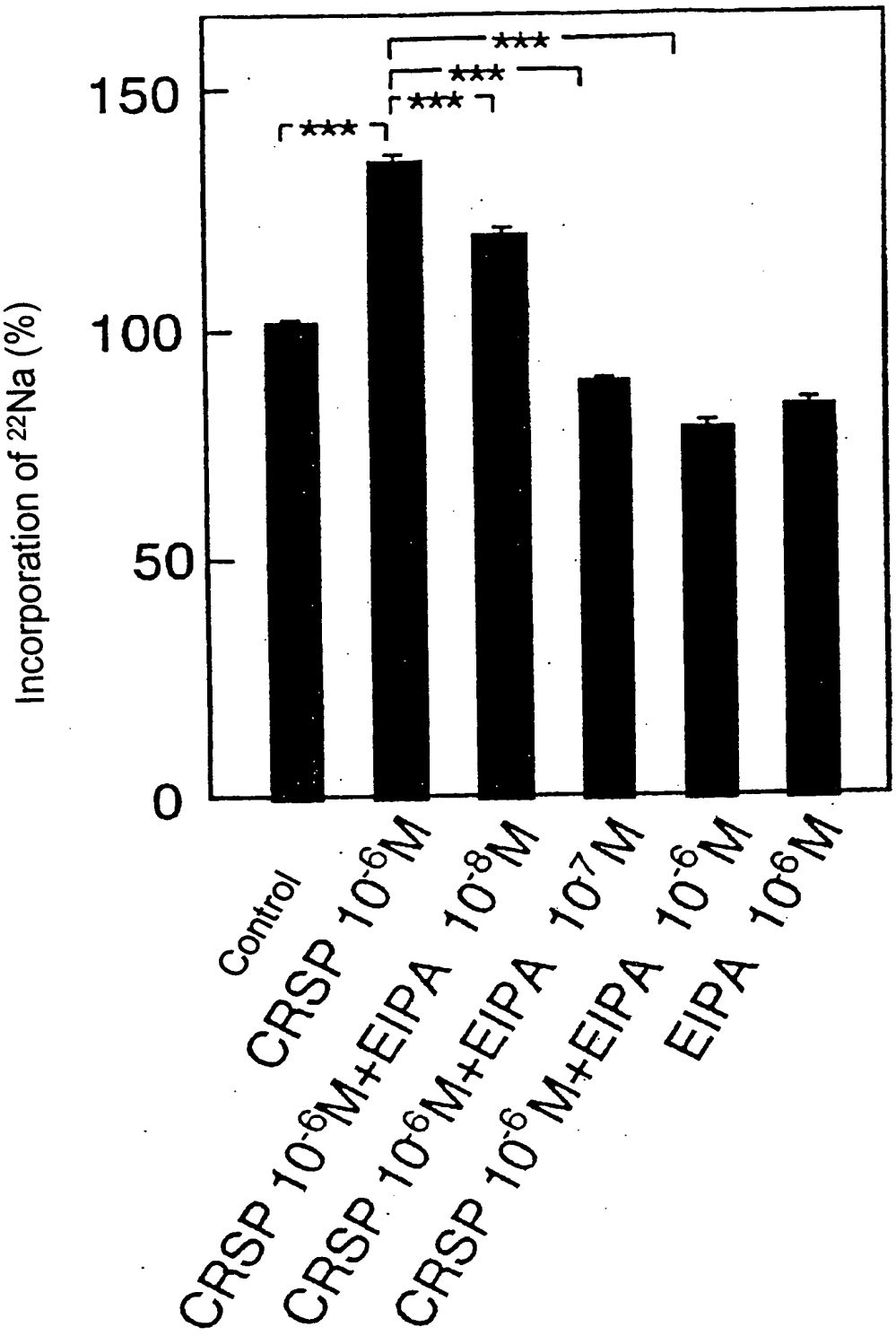

Incorporation of ^{22}Na (%)
150
100
50
0
***
***
***
***
Control
CRSP 10^{-6}M
CRSP 10^{-6}M+EIPA 10^{-8}M
CRSP 10^{-6}M+EIPA 10^{-7}M
CRSP 10^{-6}M+EIPA 10^{-6}M
EIPA 10^{-6}M

Fig. 7

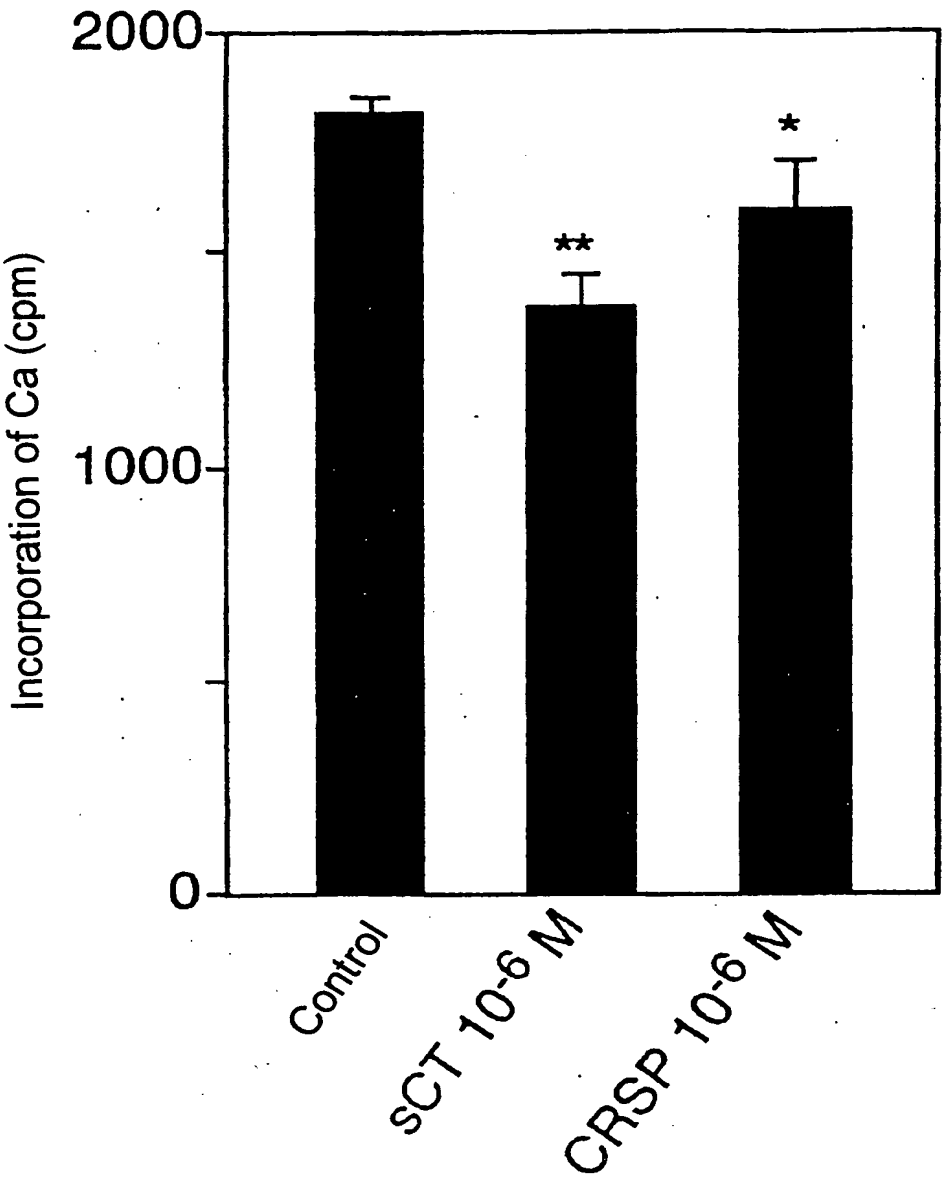

2000
1000
0
Incorporation of Ca (cpm)
**
*
Control
sCT 10-6 M
CRSP 10-6 M

Fig. 8

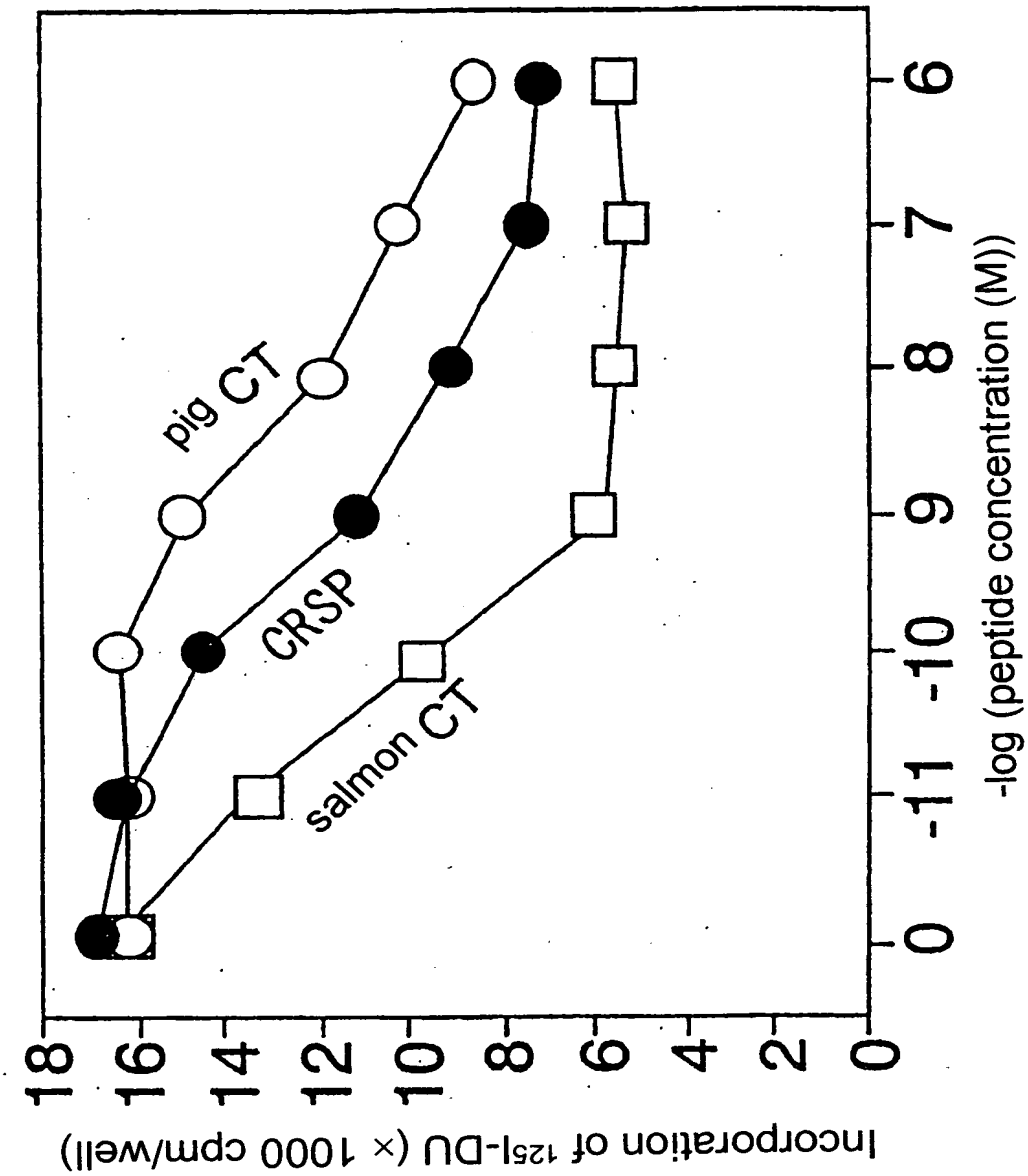

pig CT
CRSP
salmon CT
Incorporation of 125I-DU (× 1000 cpm/well)
0
2
4
6
8
10
12
14
16
18
-log (peptide concentration (M))
0
-11
-10
9
8
7
6

Fig. 9

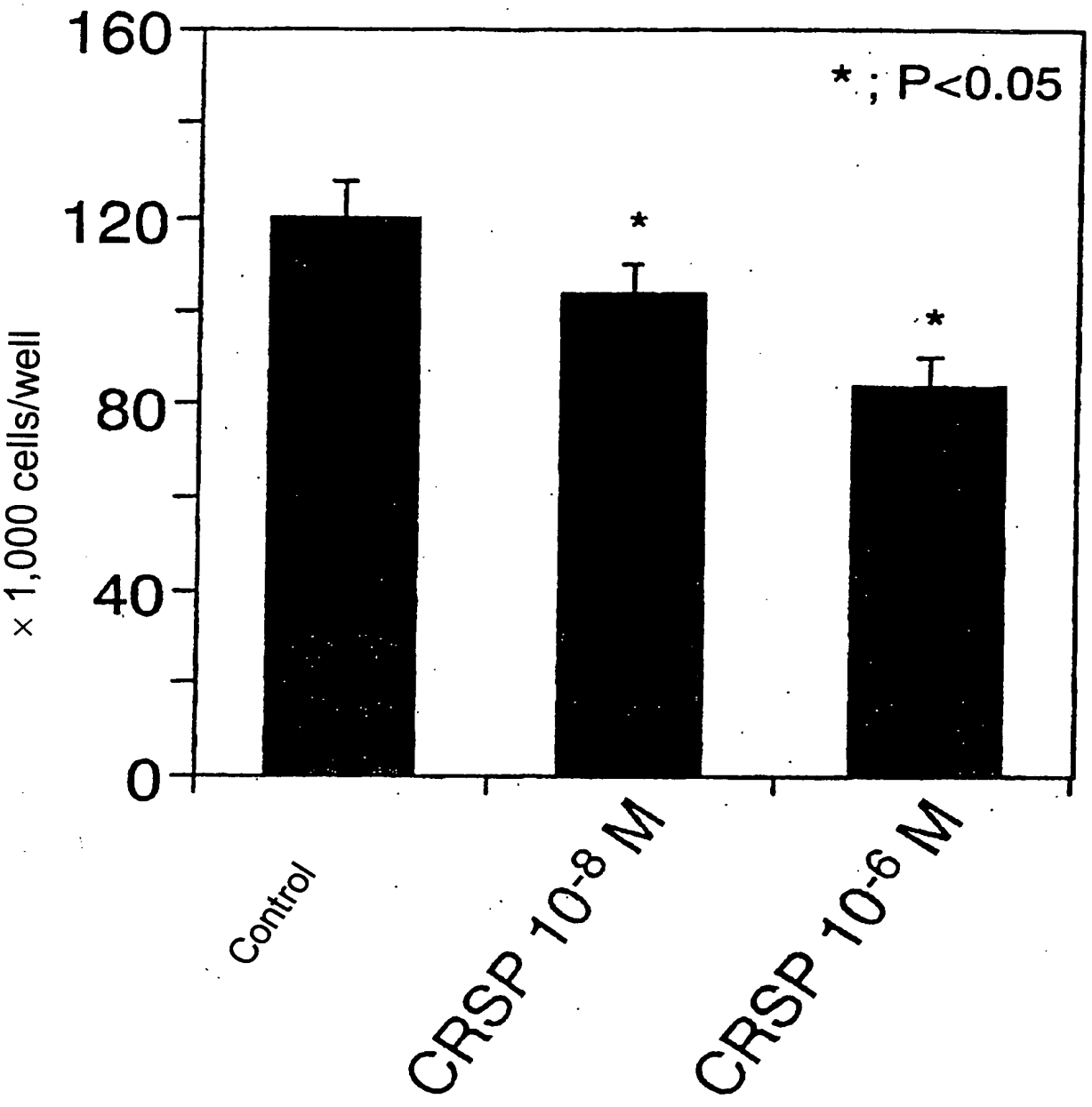

160
120
80
40
0
× 1,000 cells/well
*; P<0.05
*
*
Control
CRSP 10-8 M
CRSP 10-6 M

Fig. 10

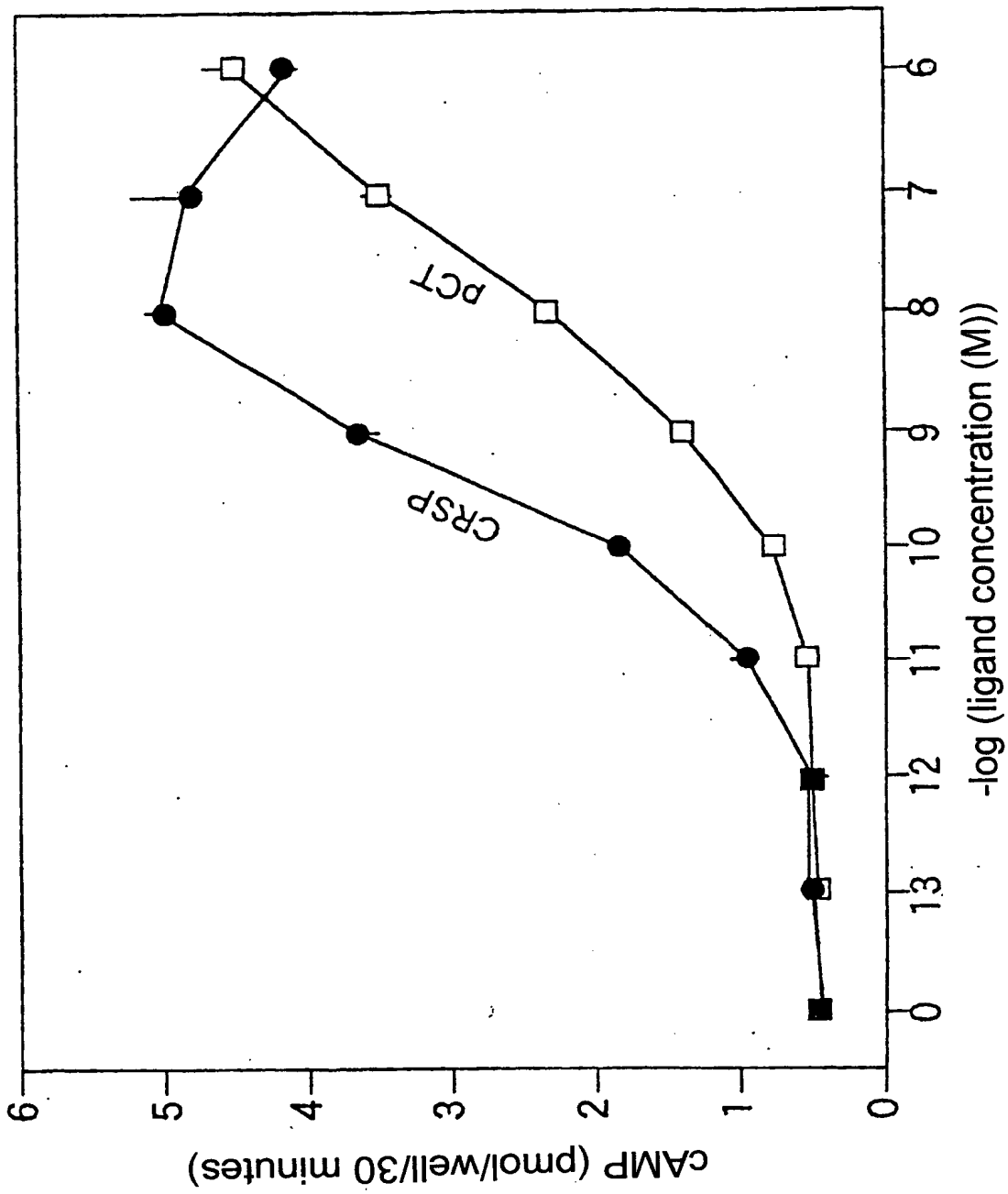

cAMP (pmol/well/30 minutes)
0
1
2
3
4
5
6
-log (ligand concentration (M))
0
13
12
11
10
9
8
7
6
pCT
CRSP

Fig. 11

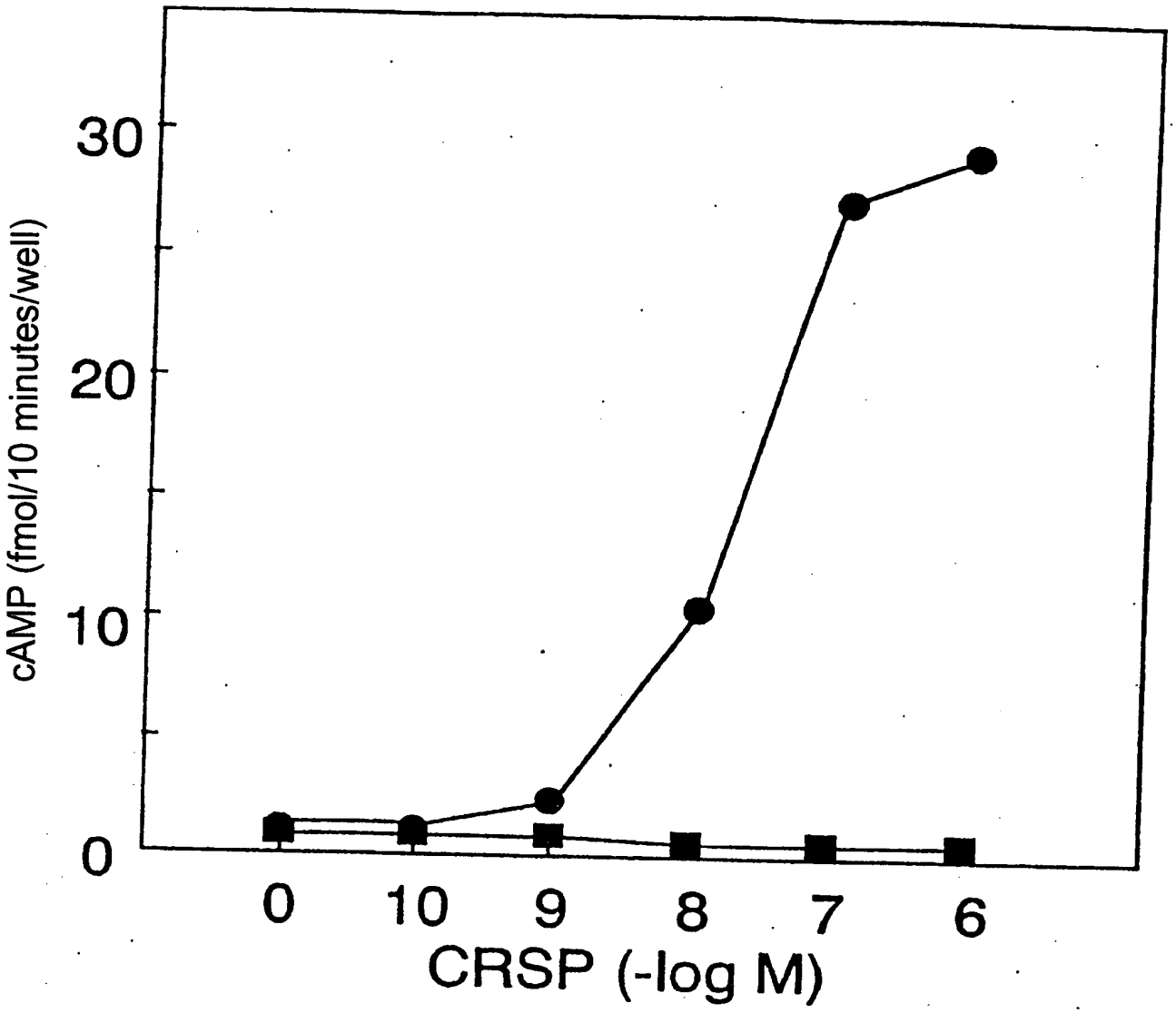


Fig. 12

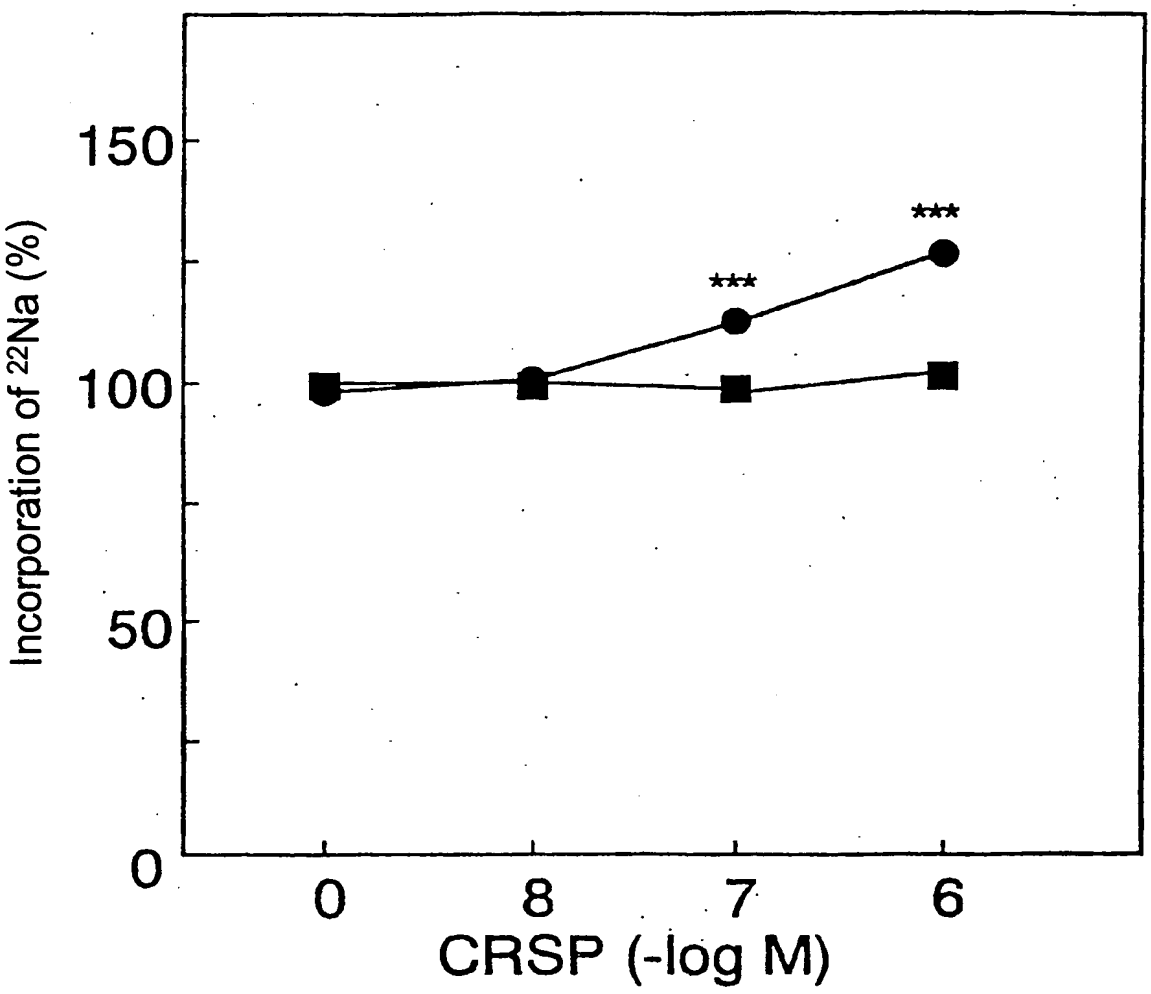


Fig. 13

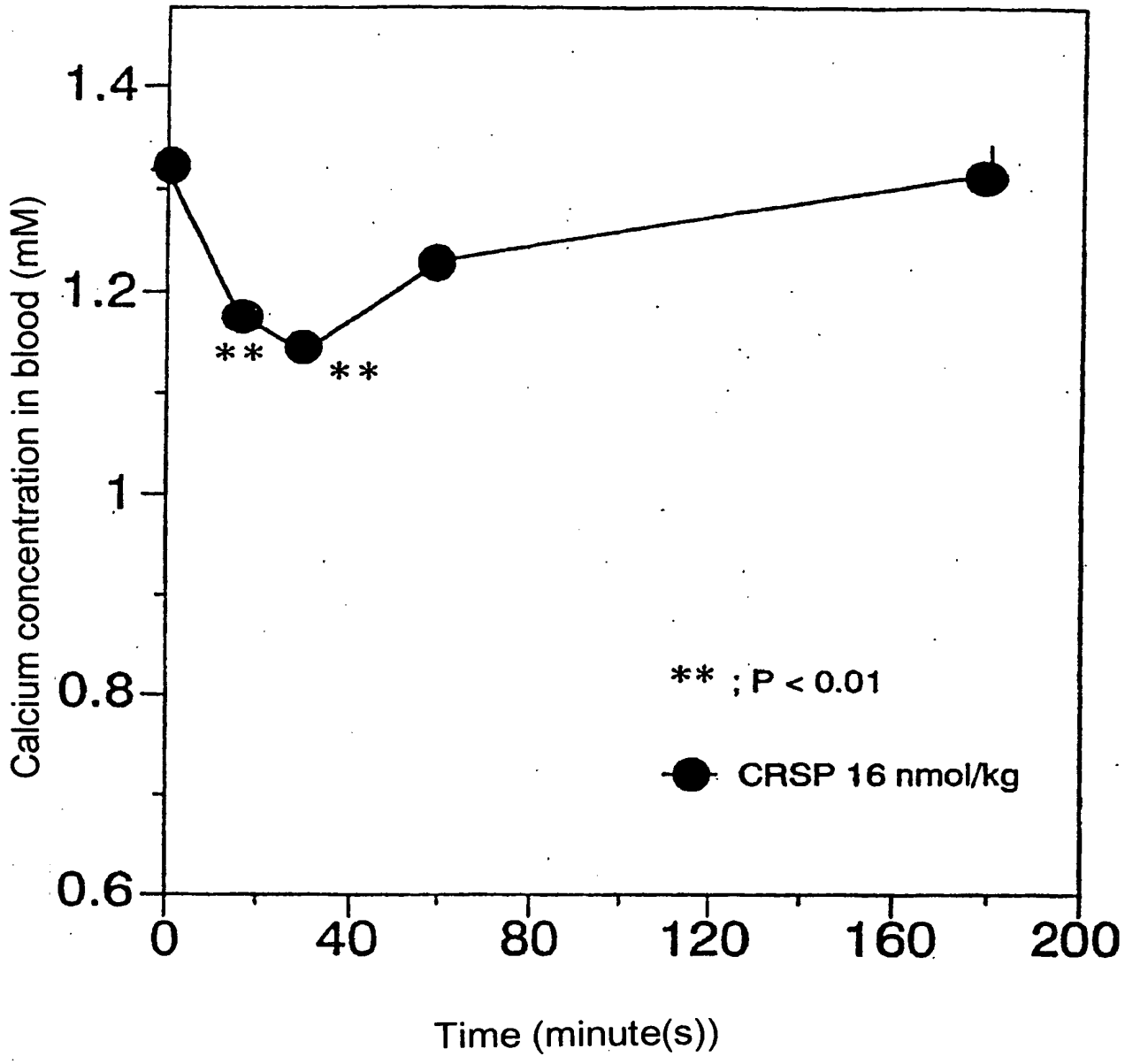

1.4
1.2
1
0.8
0.6
Calcium concentration in blood (mM)
**
**
** ; P < 0.01
CRSP 16 nmol/kg
0
40
80
120
160
200
Time (minute(s))

Fig. 14

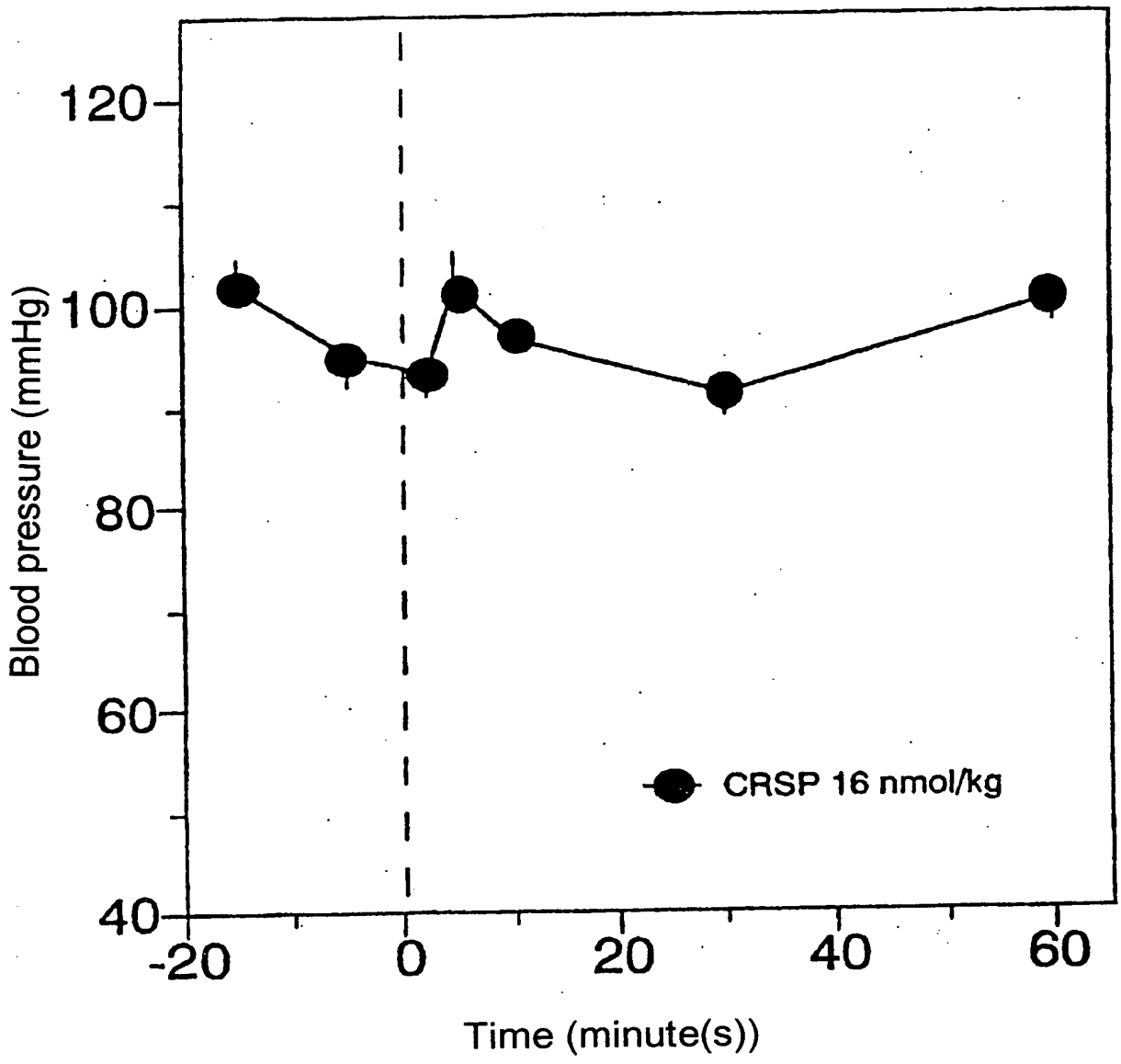

120
100
80
60
40
Blood pressure (mmHg)
-20
0
20
40
60
Time (minute(s))
CRSP 16 nmol/kg

Fig. 15

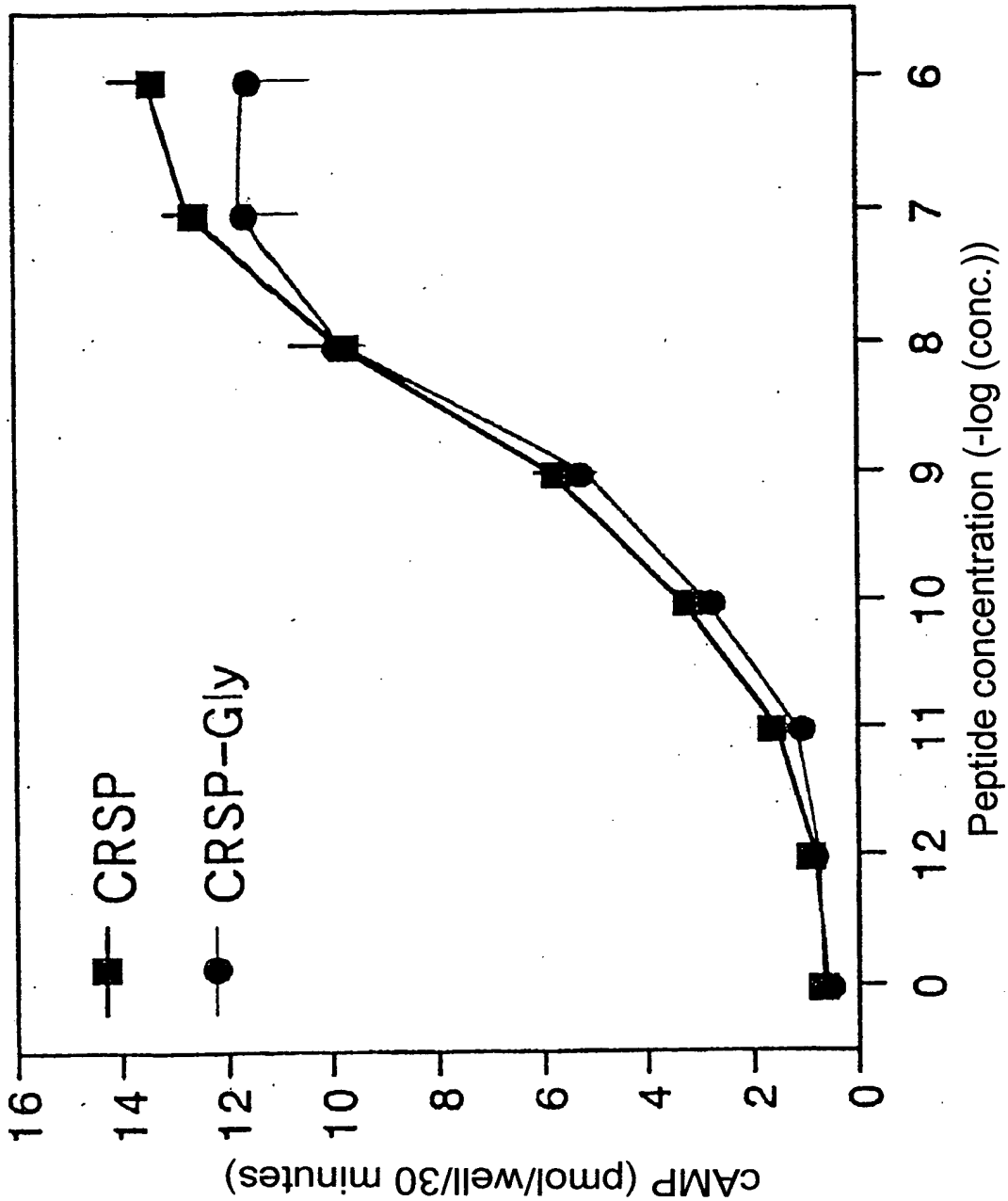

cAMP (pmol/well/30 minutes)
0
2
4
6
8
10
12
14
16
Peptide concentration (-log (conc.))
0
12
11
10
9
8
7
6
CRSP
CRSP-Gly

Fig. 16

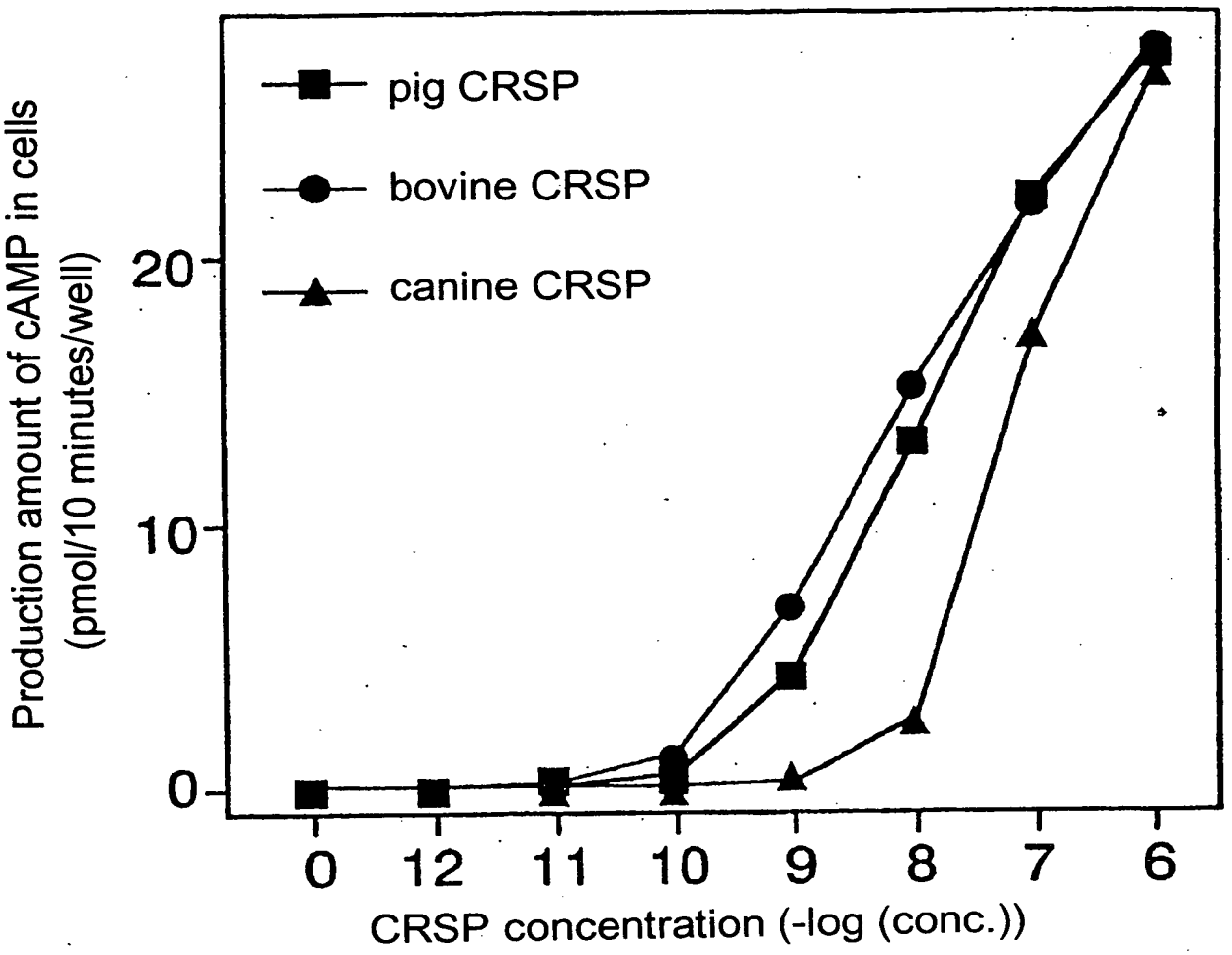

pig CRSP
bovine CRSP
canine CRSP
Production amount of cAMP in cells
(pmol/10 minutes/well)
20
10
0
0
12
11
10
9
8
7
6
CRSP concentration (-log (conc.))

Fig. 17

```
CTCGAGGATCCTGCCTCTTGTTTCCCACAAATCCTGCCTTCCTGTGCTTGATTCCAGCTG      60
CCTGAATCAGACCCCCTGCTTGGGCACAGAATCATCAACCTGCTGCGCATTAACCTCCCA     120
AACCGCACTTGGACATGGTAGTCTTAGGGGACCGGGGATGCCTTGTAATGCTGGACTCTG     180
CTCTACAAAGATCACATAGCTGGGGATGGAGAGGGATGTGAGCCTGCGAAACCGAACAGG     240
TAAAGTTTACCATGACGTCAAACTGTCCTTAAATTCCTGCTCACTTTGCGTGTGTTTTTC     300
GTTGGTGCCCACCAACCTCCCCACCCCCTCCCACCCCCGCCATCAATGACCTCAATGCAA     360
ATACAAGTGGGGTGGTCCTGTTGGATGCTCCAGGTTCTGGACGCAAGTAGTGACACAATC     420
CTGGGGCTCAGGATCTTTCCTCTCATTGGTTGCCTGGAGCTCTGGGACCACCCCAGATTC     480
AGAGCGGCGGGAATAAGAGCAGCTGCTGGTGCGGGGAAGGGTTAGAGGCACTACCCACCT     540
CAAGTGTCTCTGCCGCTTCTTCCACAGTGCCATCGCCTGACGCCAACGCTGCTGCCTCTG     600
CTCCCTCCTCTGCTCCAGTCCACCTGGTTCCTGCTGCCCGGTAAGCCCGGAGATTCCTGC     660
TAAGCTGTGGTTCTGTTTCTCTCTCCCTCTCCTCCCTTCCCTCTCTCTCCATTGGATTTT     720
CTTAGCTGATCTCTTTTCCCGTCTCAAAGTTCCTGTCCACTTCTCTCTGGGTCTCTTCAT     780
CCTGTAATATGCCTTACTGCGCAATTCATTCTAGGCTCCTTTCACAGGTAACTCTGGATG     840
GTCTCAGTTCGGGGATTCCCTGCTCTACTCTTCCTGAGCTGAGCTGGGCTCCAGTCTTGT     900
CCCCGCAGCAGACGTGCTTAGGTCCGTGTTGGGATTTTGGAGCTCTCCAGGCACTTCAGG     960
GAGAGGAGGATGCAGGAATAGCTTTGAGCAGAAGAAACTTTCATGGATCCCATCTCCTCT    1020
TACCTACAAGGATCGCTGGAAATGGGGTCGGGACCTGGGACAGTGCAAATGGGTGGCAAA    1080
TAGGTGCAATGACTGAGGGGAAAGTAGCTATTAAACGCAAGCCCCAGTTGAAGGTTCTGG    1140
GAACTCCCCCTCCCGCACCGCCACCCCATTTAATCTTGGGTCCCAATTTAAGGCTGTACC    1200
AGCTTGTTTCTTACAGGGTGCTCTTTGCCAGAGTATGGAGCAGCTGGACAGTAAAATTTG    1260
GTTCTTCAGTTTCTCAGGGATTCCAACTGCAGAGATATGTCCTCCCAACTCCCCTTCCCC    1320
CCAGCCAGGTATAAGCAAAAATCAGGCATCAGGAGAGATGCTGATGGGTTGCACTATGGG    1380
AAAAGCTGTGGTGACAGGTACTGCGAGTCTGTCCTCCAGGAGTCCCGGCCAACAGGTTGA    1440
AGGTGAGAGTGTGGGTGTGCTGGGCAGGGGGCTATGGACGGAGACCTCCTCACCCAGTTG    1500
TCCTGCTAGGCTTCTTTGCTAAACCAAACATGTTGCAGGCTCACTGGATCTTCCAGCAGT    1560
CCACTTGGCTGAGGAGGAAATGATGGTGAAAGGAAAGGACACGAGCAGCCTGAAGCCAGG    1620
AAGCCAGGGAGTTGGAGGCAGAGGCAGGAGCAGAGCCCAGGTCTGTGGGCTCAATGAACT    1680
TGGAACTGCTACAGGTGGTGACATTGTTCTTCCCTTGCAGAGGGGCACCATGGGCTTCTG    1740
                                                  MetGlyPheTr

GAAATTTCCGCCCTTCCTGGTTCTCAGCATCCTGGTCCTGTACCAGGCAGGCATGTTCCA    1800
pLysPheProProPheLeuValLeuSerIleLeuValLeuTyrGlnAlaGlyMetPheHi

CACAGCACCAATGAGGTAAGACAGCCCTGCCAACAAGCACACTCACTTGATGAGAATGTA    1860
sThrAlaProMetAr

ATATAAACGTGTATATAAATTTATTATAAGGTGGCTCTGTAGAACAATGGATAGTGCCTT    1920
GCGCTCCTATAAGTTTATCATAAGCTTTATGTGTACACAAAGTTTGTAAATAGACATAAG    1980
ATATACAGTACTCATGATTGTAAATTTTATATAACTTATCAAACCTCACAGCATGCTTTT    2040
TTGTTTTCATCAAATATTTGTACCTTTAGCACACGTATATGCTCATATTACCATAATTTA    2100
AGAAATGGATTGTATCCAATTTGCCAAATACTTTGCTAGTAAATTTGTTATTAAATCTGA    2160
TATGGGATCTACACATCTCATTTTTCACCTTCATTCAAACTGCATTAAGCTAAAATTATT    2220
TTCCCATTCAAACTATCAGAAACCAGGCAACCTGGCTGTTTATCCTGGGGAGGGGCAGGC    2280
AGGAGATCAGAACCTGTTTTTAGGCTTGCTTCCCCTCCTTAGGTCTGCCTTTGGGAGCCC    2340
                                                  gSerAlaPheGlySerPr
```

Fig. 17

(continued)

```
TTTTGATCCTGCTACCCTCTCTGAGGAGGAATCACGCCTCCTTTTGGCTGCAATGGTGAA  2400
oPheAspProAlaThrLeuSerGluGluGluSerArgLeuLeuLeuAlaAlaMetValAs

TGACTATGAGCAGATGAAGGCCCGTGAGATGCAGAAGCAGAGGGCACAGGGCTCCGGGTA  2460
nAspTyrGluGlnMetLysAlaArgGluMetGlnLysGlnArgAlaGlnGlySerGl

AGGTTCCCTGCCCAAGGACAACAGGGCATCCCTTTCTTCCTCTGGTCAGGCCCAGGAAGG  2520
CATATTTTAAAGTCACTTTTGAGTTTTCTGACCCCCCTGGACATGTCTGTGGGATGATTA  2580
TGGCATTTCCCCTGACGGCCTAGGATTTTCTGCTGTGATGACCTTTTCTAGCAGAAATAC  2640
TCAAGGTTCACTGGTCCTCTCAAGGCAGTAGTCTTCCATGACGATTCTGTCGTACAGCAC  2700
CTGCACTCAACCTCTCACTGACGGGCCTTTTCTTTCTTTATCCCACAAATCAGCATCAGT  2760
                                                      yIleSer

GTCCAGAAGAGATCCTGCAACACTGCCACCTGCATGACCCATCGGCTGGTGGGCTTGCTC  2820
ValGlnLysArgSerCysAsnThrAlaThrCysMetThrHisArgLeuValGlyLeuLeu

AGCAGATCTGGGAGCATGGTGAGGAGCAACCTGTTGCCCACCAAGATGGGCTTCAAAGTC  2880
SerArgSerGlySerMetValArgSerAsnLeuLeuProThrLysMetGlyPheLysVal

TTTGGTGGGCGCCGCAGGAACTTTTGGATCTGAGCAGTGGGATGATTCCAGGAGGAAGGT  2940
PheGlyGlyArgArgArgAsnPheTrpIle***

GACTGCCCTTTTTGTACCTTCGGGTGGGAGGACAGAGGACTGGGTATTGCAGGGGTGCAT  3000
TCCACACCCTAACCCTCTGTGAGCGCATGGGGGTAAAACCTCCACATGGCAAGGTGCCCA  3060
CACCAGTGTCTGGAGAAAGGACTGATAATCCCTATAACTGAAACATTGGGCTCTTTCTCT  3120
CTGTTTCTCCAGTCTCTCCCTGTGACACTGACATCATCTGCCAGGAAATATAGACCCTGT  3180
TTACTTAAAACACTGTTCCCTGGGTATTAATTGGGGTCCAGCTCTAGCATTAGAATTTGA  3240
AAGGTAATGACCCTACCCTTTTGGAGCATACCTTACAATGTTATGAACTTGGAGCATAGA  3300
CTCGGATTCAAATACTGTGTCTGTCTTCCACTAACTGTGACCATAGGCAAGTATGCCTCT  3360
GAGCCTCAGCTTCTCCTTGTAACTTGAAGGCAACAATAGTATCCTCAATATAAAAATTAA  3420
TTAGTATAACATATGACAAGAGCCTGTTAACTAAGAATTAATAACATTCTGTTACTTTTT  3480
TCCCTCCTAGGTTACTATGACTCTGAACTCTACTTCGTTTAATTTACAATGAAAGCAACC  3540
TACTAAAAAATAGCATGGAAGACATCCATGTATGCATGCTTCTGGAAACTGAAAACACTC  3600
TTTTCCTTGAAATAAACTAAAACTAAATGCAAAATAAAATCAATGCATCAATGCAGTTAC  3660
CTTGTGTGCATCTTTTGTGTATATGATTCTATAATATGATGCATGTCTCATTAGGTTTAA  3720
TGGTAGCAAATCTGGCCCCTGTCAGCCAACCTGTTGGTGGGGGCAGCTCTGCTAAACCTC  3780
AGGGTCACATGAATTC                                               3796
```

Fig. 18

```
GGATCCACTAGTTCTAGATAAAATGGACAAATACCTAGAAACAGAAGACCTACCAAGATG     60
GAAGGATGAAGAAATAGAAAATTCAAATACACCTATGACTAGGAAGGAGAATGAAGCATT    120
AATCCAAAATCTTCCAACAAAGAAAAGCCCTGGATACGATGGCCTCATTGGTGAATAGTA    180
CCAGACATTTAAAGAAAACGAATACCAATCCTTGTCAAACTTTTCCAAAAACCTGAAGAG    240
AAAGGACACACCCTAACCTATTCTATGAGGCAGGCCAACATTACTCTGATACCAAAGATG    300
GAGAAAGATTCTGCAAGGAGAAAACCCCTACAGACAAAATCCTTTATGACATGGATGTGG    360
AAACCCTCAACAGTATGCTAGGGAATTGAATTCAGAAGCGTATTAAAAGGATCCTACAAC    420
ATGACCAAGTGGGATGAATTTCTGGAATGCAAGGATGATTCAAAATATGAAAATTGATCA    480
AAGTGTTATATCACAATAATGGAATGTAGGGAAAAACACACCTGATTATTTCCACTGATA    540
CAGAAAATTATTTAGTAAAATTCAATACCTTTTCAGGATTAAAAACAAAAACTAGGTATA    600
GAAGGAGACTGCCTCAGCACAATACAACTATATATGAAAAACCAACACCAACACCATAAT    660
CCAGGGTGGAAAACTGAAAGCTTTTCCCCTAAGATCTGGAAGAAAATGGAAAAAAATTTT    720
TAAGAATTTTCAGACAGATTTGGGTCTCTGGTACACTCTGAGAAATCATCTTTTAGAATT    780
TTTTTTTTTTAAAAATAAGCACAAGAATTTCATTTAAAAGAAGGGAAATAACATAGCCTT    840
CAGAGTTTATCAGGAGGTGTAATTTTTTTTTCCACACTAGATTGTGGCTACCTGATGCTA    900
ATTTTGAGGTTTAAACATAATGAAATAAGATTGTACAGCCAAGTGCCAGCTAGTCATGGA    960
ACTTTTACCTCAGTACTGTTTAGTGCTTCAGTCCTAAGAAGTTTCAGGGAGGGCTGCGTG   1020
CAATACAAGTAATCGGTACTTGCTGAAGGTCTAAAATTTCGAGTGCACTTGGTAAATCAG   1080
GGATGGGCGCAGAGGAGACTGGTTCTGTAACTCAGACTAGTGAACCCTAGAATTTAGAAA   1140
GGGTACTTTTGTGCTCCAAGCAAATCCTGTTCTACCTAACTAGGTCCAAATGCTCTGCAG   1200
GCTGTAGTTAGAGCCCTCTCATAGCAGGGAGACTGCCTTGGTGAATCTGCCAGAGGAAAT   1260
GAATTTCCATTCACATTCATTCAACAAACATTGGGCGAGTGCCACCTCATGTGCAAAACA   1320
TGGTGCTAAGTGCTAAAGAAAAGATGTTGTTTTGTAAACTTACCCGCAGCTCAGAGCCAG   1380
GACTTCTTGGAAAGTCAGAGGACTTGAGGAAGGAGTTCATCTCAGCCCCTCCCTCACTGG   1440
AGAGACTGGCTTTTCTTTCCAAGTAAAGCTTAAAACTGCTGGAGGCTAAGTTAGCACCCT   1500
CTGGGGGCAGACCCTGATTCCTGCCTCTCATCCCCAGCCCTTTGTGTGTGGGCGCCAAAG   1560
ATTTCTGAGTGAGGAATGAATGTTGGCTTTGAACAGGAAAGGCACAAGTGGCAGCCAAGG   1620
GTAGAATGCTGAGCCTACAAATTAACATAGTTACAAATTTGTCTTCTAAAGGAGTCGTTT   1680
CTTAGCCATAGTGCAGCCACCTTTGCATTGATCAAAACTGTGGTTCTTCCAATGAAAAAA   1740
GACATCCCCAGACACACATACTTACAAATGATTTCAGAAGATTGATAGGTCGGAAATCTC   1800
AGGTTTTGGATTTTATTTGCAAAAGCGTTTTGCGCCTGAGTTTTAAACTTTTTTTTTTTT   1860
TTTTTTTTTTTGTATTTTTTCACTTCTAGGGCGGCTTCGGCGGCATATGGAAATTCCCAG   1920
```

Fig. 18

(continued)

```
GCTAGGGGTCTAATAGGCGCCATAGCCACCGGCCTACGCCAGAGCTACTGCAACGCTGGA 1980
TCCGAGCCGCATCTGCAACCTACACCACAACTCACGGCAATGCCGGATCGTTAACCCACT 2040
GAGCAAGGCCAGGGATCGAACCCGCAACCTCATGGTTCTTACTCAGATTCGTTAACCACT 2100
GCGCCACGACGGCCACTCCAACCTACCAGACTCTTAATTAAGTAGCAGAGTCCAATTTAC 2160
ATGCCGCACCACATCTGTTACCCCGAGTTAGCGAACTTGGTCTTGGAACTAACTCCTCAC 2220
GGAAAGCCAAGCCGAGTACTCATAATTATAGTGCTGAACCCCCAAACCCTGGTCTGGCCT 2280
GTGCACCCAATTTTTGCTTGTAGTAGAAACCAGGATTTACGGAGCCCGAGCAGTCCGCCA 2340
TCCTGAACTCTTCTCTTTCTCACCTTGCCTTCATCCTGGAGTGCACCTGCCCTCTATGAA 2400
CCAGTTTTTCCGTTCCCTTGGTCTCCCGATCCGTTGTCTATCCTGAGGAGAGCGAGATGC 2460
AAGCACCCGATTCCCTAGCCCCAATATTTTATTCTCTTGCGAAGGAGAAAAGTTGAATAA 2520
GGGTATCTTGTAAATGAGATGTTCCGAGTCCAGAGAGCACAAACCGGCAAGGGGAACAGA 2580
TGTGCCGCGAGGCAGGTGTGCGGAAAGATATAGAGAAGGCTCAGGTTCGGACCTGTGGCT 2640
CAGGTCACACTCATGGCAGAGTTCGGTTTAATTTCGGCTCTGCCTGGGGGAACCACTTAA 2700
CTGGGGTCCTTGCTGCCCTCCACCGGCCCCCGATGCTGTTGCAGCGTTTGCCGCGCTGGA 2760
GGGTCTGTACAGGCTGCTGCGGTTTATCGCTGTGTGCTCAGACACGGTGATCCTGAGCAG 2820
CATCCGAACTGGATTGGGGTAGATGTGGGCACAGGGCTGGAATCACAGGTCACTGGAACA 2880
TCTTGGCAAACAGCAGCCGGAAGCAAGGGGCAGCTGGGCAAATGGTTCTGGGACATTGAT 2940
GGGCTTAGATGATGAATGGTGGGGCTGGAGGTCGGCTTGGCGGCTTGGGAAGCATCTATG 3000
CCGTGCACGTCCCTGCCCAAGCCCAGTAGGGCACCATCTTTCCCCATATGGTGGACCGAC 3060
CACCCAGCGCGACTCCAGACATCCGCACAGAGGTGGGGATTGGGCAAATGGATCGCGATC 3120
GCACAGAATCCCCTCTGCACTTCCCTGGTAAGCTCTTCTCGATCCCTCCCTGGGTGGAGA 3180
GCAGGTACATGGCTACTAATGATACCACTCCTTGAAGACGGGAATATGATGCCCCGTTCC 3240
AAAAATTAATATATTGAGGTGCTAGAAGACACTAGCCCGATGATCTTACTACCTAGAAAA 3300
GGCACAGCTGGAACAAAGTTTCCGTGTGACAAAGACTGTGATCCTGCCTCTTGTTTCCCA 3360
CAAATCCTGCCTTCCTGTGCTTGATTCCAGCTGCCTGAATCAGACCCCCTGCTTGGGCAC 3420
AGAATCATCAACCTGCTGCGCATTAACCTCCCAAACCGCACTTGGACATGGTAGTCTTAG 3480
GGGACCGGGGATGCCTTGTAACGCTGGACTCTGCTCTACAAAGATCACATAGCTGGGGAT 3540
GGAGAGGGATGTGAGCCTGCGAAACCGAACAGGTAAAGTTTACCATGACGTCAAACTGTC 3600
CTTAAATTCCTGCTCACTTTGCGTGTGTTTTTCGTTGGTGCCCACCAACCTCCCCACCCC 3660
CTCCCACCCCCGCCATCAATGACCTCAATGCAAATACAAGTGGGGTGGTCCTGTTGGATG 3720
CTCCAGGTTCTGGACGCAAGTAGTGACACAATCCTGGGGCTCAGGATCTTTCCTCTCATT 3780
GGTTGCCTGGAGCTCTGGGACCACCCCAGATTCAGAGCGGCGGGAATAAGAGCAGCTGCT 3840
```

Fig. 19

```
GGTGCGGGGAAGGGTTAGAGGCACTACCCACCTCAAGTGTCTCTGCCGCTTCTTCCACAG   3900
TGCCATCGCCTGACGCCAACGCTGCTGCCTCTGCTCCCTCCTCTGCTCCAGTCCACCTGG   3960
TTCCTGCTGCCCGGTAAGCCCGGAGATTCCTGCTAAGCTGTGGTTCTGTTTCTCTCTCCC   4020
TCTCCTCCCTTCCCTCTCTCTCCATTGGATTTTCTTAGCTGATCTCTTTTCCCGTCTCAA   4080
AGTTCCTGTCCACTTCTCTCTGGGTCTCTTCATCCTGTAATATGCCTTACTGCGCAATTC   4140
ATTCTAGGCTCCTTTCACAGGTAACTCTGGATGGTCTCAGTTCGGGGATTCCCTGCTCTA   4200
CTCTTCCTGAGCTGAGCTGGGCTCCAGTCTTGTCCCCGCAGCAGACGTGCTTAGGTCCGT   4260
GTTGGGATTTTGGAGCTCTCCAGGCACTTCAGGGAGAGGAGGATGCAGGAATAGCTTTGA   4320
GCAGAAGAAACTTTCATGGATCCCATCTCCTCTTACCTACAAGGATCGCTGGAAATGGGG   4380
TCGGGACCTGGGACAGTGCAAATGGGTGGCAAATAGGTGCAATGACTGAGGGGAAAGTAG   4440
CTATTAAACGCAAGCCCCAGTTGAAGGTTCTGGGAACTCCCCCTCCCGCACCGCCACCCC   4500
ATTTAATCTTGGGTCCCAATTTAAGGCTGTACCGGCTTGTTTCTTACAGGGTGCTCTTTG   4560
CCAGAGTATGGAGCAGCTGGACAGTAAAATTTGGTTCTTCAGTTTCTCAGGGATTCCAAC   4620
TGCAGAGATATGTCCTCCCAACTCCCCTTCCCCCCAGCCAGGTATAAGCAAAAATCAGGC   4680
ATCAGGAGAGATGCTGATGGGTTGCACTATGGGAAAAGCTGTGGTGACAGGTACTGTGAG   4740
TCTGTCCTCCAGGAGTCCCGGCCAACAGGTTGAAGGTGAGAGTGTGGGTGTGCTGGGCAG   4800
GGGGCTATGGACGGAGACCTTCTCACCCAGTTGTCCTGCTAGGCTTCTTTGCTAAACCAA   4860
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GAAAGGAAAGGACACGAGCAGCCTGAAGCCAGGAAGCCAGGGAGTTGGAGGCAGAGGCAG   4980
GAGCAGAGCCCAGGTCTGTGGGCTCAATGAACTTGGAACTGCTACAGGTGGTGACATTGT   5040
TCTTCCCTTGCAGAGGGGCACCATGGGCTTCTGGAAATTTCCGCCCTTCCTGGTTCTCAG   5100
                MetGlyPheTrpLysPheProProPheLeuValLeuSe

CATCCTGGTCCTGTACCAGGCAGGCATGTTCCACACAGCACCCGTGAGGTAAGACAGCAC   5160
rIleLeuValLeuTyrGlnAlaGlyMetPheHisThrAlaProValAr

TGGTGGCAGTGCTCTCGCTTCCCACGGCCCCCGGAATCATATAGTTCTGTATTGTGAGTT   5220
GTGCTGTGGTGAGTCTGGCTCTTGGTGGGCTTCTGTGTATAGGGGGTGTGGGGTCCTAAT   5280
GTATGAATATAGTCATGTATATAAGTTTATTATAAATATTTTGTGATCCAAGATAATATC   5340
ACAAAGTTTACAAATAAATAGAAGATATACAGTATTCACTATAAATTTCTAAACTCACTG   5400
AACCTTACAGCATGTTTTTGTTGCTTTTTATGAAATGTTTATAACTTTAGCAAACCTATA   5460
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GGAAGTGGCAGAAACCAGGAAATCTGGCTGCTTATCCTAGGGCTGTGGTAGGCTCAGAGC   5880
GCATGTTGGGCTTGCTTTCCCTTCCCAGATTGCCTTTGGAGAGCAGCTTTGATTCTGCCA   5940
                gLeuProLeuGluSerSerPheAspSerAlaT

CTCTCACAGAGGAGGAAGTGTCCCTTCTACTGGTTGCAATGGTGAAGGATTATGTGCAGA   6000
hrLeuThrGluGluGluValSerLeuLeuLeuValAlaMetValLysAspTyrValGlnM
```

Fig. 19

(continued)

```
TGAAGGCCACTGTGCTGGAGCAGGAGTCAGAGGACTTCAGGTCAGTCTTTGCACCCCTCC   6060
etLysAlaThrValLeuGluGlnGluSerGluAspPheSe

CAGAATATGGCTTACCCTCTCCCTAGAGTACCAGGAAGGCATATCCTTAAGAATGAGATT   6120
TGTTATAGTGCCATAAGCCTTGATGTCCAGTCTCATAAGCCTTGGTTTATTTTTAGTTTA   6180
TTACACAGGAGAGATTGTCTATTACAGTTCTGATTTCCAGGTCCAGTAATGCAGAGCCAC   6240
CTTTGGGTTTTCTGACACCCCTGAAAATGTCTATGGGGAGTGATGATGCATTTTCCCAAA   6300
AGCCCTATGGTTTTCTGTTGGGATTTTGTGTTTAGCAGAAACATTTCAGGTTCACTGGTC   6360
CCTCTCAGAGCTGTAATTTTCCACTGATGGTCAGTCCTGGGGGGAATCACTTGCCCTCAA   6420
GCTGTCATTGGCAGGCCTTCTCTTTGTCTCCATCCTGAAAATCAGCATCACTGCCCAGGA   6480
                                                rIleThrAlaGlnGl

GAAATCCTGCAACACTGCTAGCTGTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATC   6540
uLysSerCysAsnThrAlaSerCysValThrHisLysMetThrGlyTrpLeuSerArgSe

TGGGAGCGTGGCTAAGAACAACTTCATGCCCACCAATGTGGACTCCAAAATCTTGGGCTG   6600
rGlySerValAlaLysAsnAsnPheMetProThrAsnValAspSerLysIleLeuGly**

ACGCCGCAGAGAGCCTCAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTGACTGCTC   6660
*

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CCCTCCCTGAGCCTGTACTGTAAAAAAAAATCCATAATGAAGTTGCTGACCCCATTATCC   6780
TCAGAAAGAAAAGAGAATCCTAATAGCCAAAACCCCTATAACTTAGGTTCATTTCTATTT   6840
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CTGAACCATAGCTGTGACCTATGCAGTACCTGTGGCAACACTGGATCCTTAACCCAATGT   7020
ACCACATCAGGAACTCCTAGGTCCTATTATTTAAAACACTGTTCCCTGCAGTTATAATTG   7080
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TCTTCCACTAACTATACAACCATGGGCCAGACCCTCTCTGAACCTCAGTTCTACATGAAA   7260
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TAGGTCACCAAGGAACTGAACTCTATTTCTTTTAATCTGCAATGAAAGCAATTTATTTGA   7440
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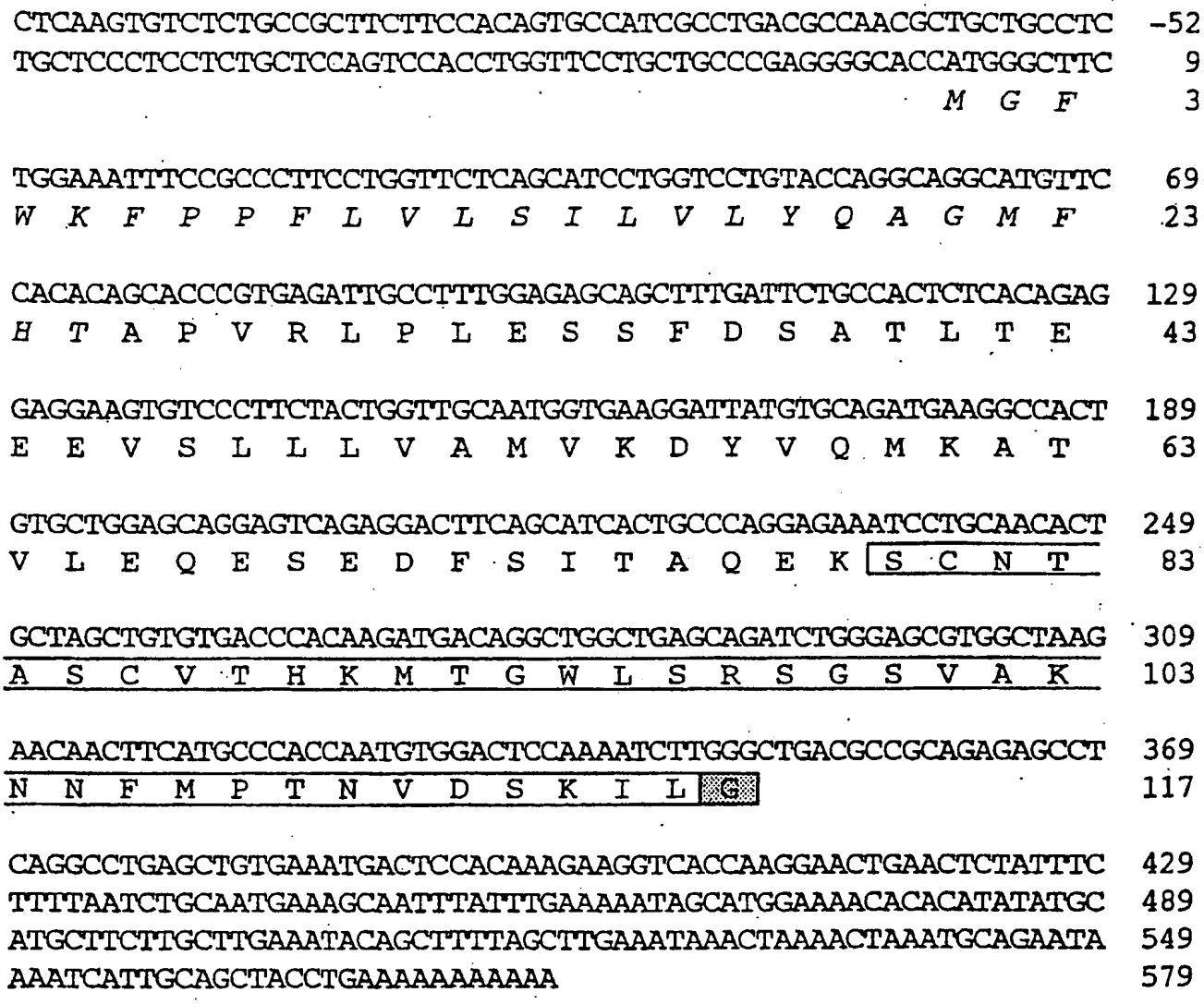
Fig. 20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W K F P P F L V L S I L V L Y Q A G M F 23
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Fig. 21

```
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TGGAAGTTCCCCCCCTTCCTGATCCTCAGCATCCTGGTCCTGTACCAAGCAGGAATGCTC   69
W  K  F  P  P  F  L  I  L  S  I  L  V  L  Y  Q  A  G  M  L     23

CATGCCGCGCCATTCAGGATGGCTTTGGGAAGCAGCTTTGATTCTGCCACACTCACGGAA  129
H  A  A  P  F  R  M  A  L  G  S  S  F  D  S  A  T  L  T  E     43

GAGGAAATGTCCCTCCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT  189
E  E  M  S  L  L  L  V  A  M  V  K  D  Y  V  Q  M  K  A  T     63

GTGCTGGAGCAGGAGACAGAGGACTTCAGCATCACCACCCAGGAGAGATCCTGCAACACT  249
V  L  E  Q  E  T  E  D  F  S  I  T  T  Q  E  R  S  C  N  T     83

GCCATCTGTGTGACCCACAAGATGGCAGGCTGGCTGAGCAGATCTGGGAGCGTGGTTAAG  309
A  I  C  V  T  H  K  M  A  G  W  L  S  R  S  G  S  V  V  K    103

AACAACTTCATGCCCATCAACATGGGCTCCAAAGTCTTGGGCCGGCGCCGCAGACAGCCT  369
N  N  F  M  P  I  N  M  G  S  K  V  L  G  R  R  R  R  Q  P    123

CAGGCCTGAGCTGTGAAATGACTCTAAAAAGAAGTTGAACTCAAGTTGCTTTCACTGCAA  429
Q  A  *                                                        125

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GAATAAAATCATTGCAGTTACCTGA                                      574
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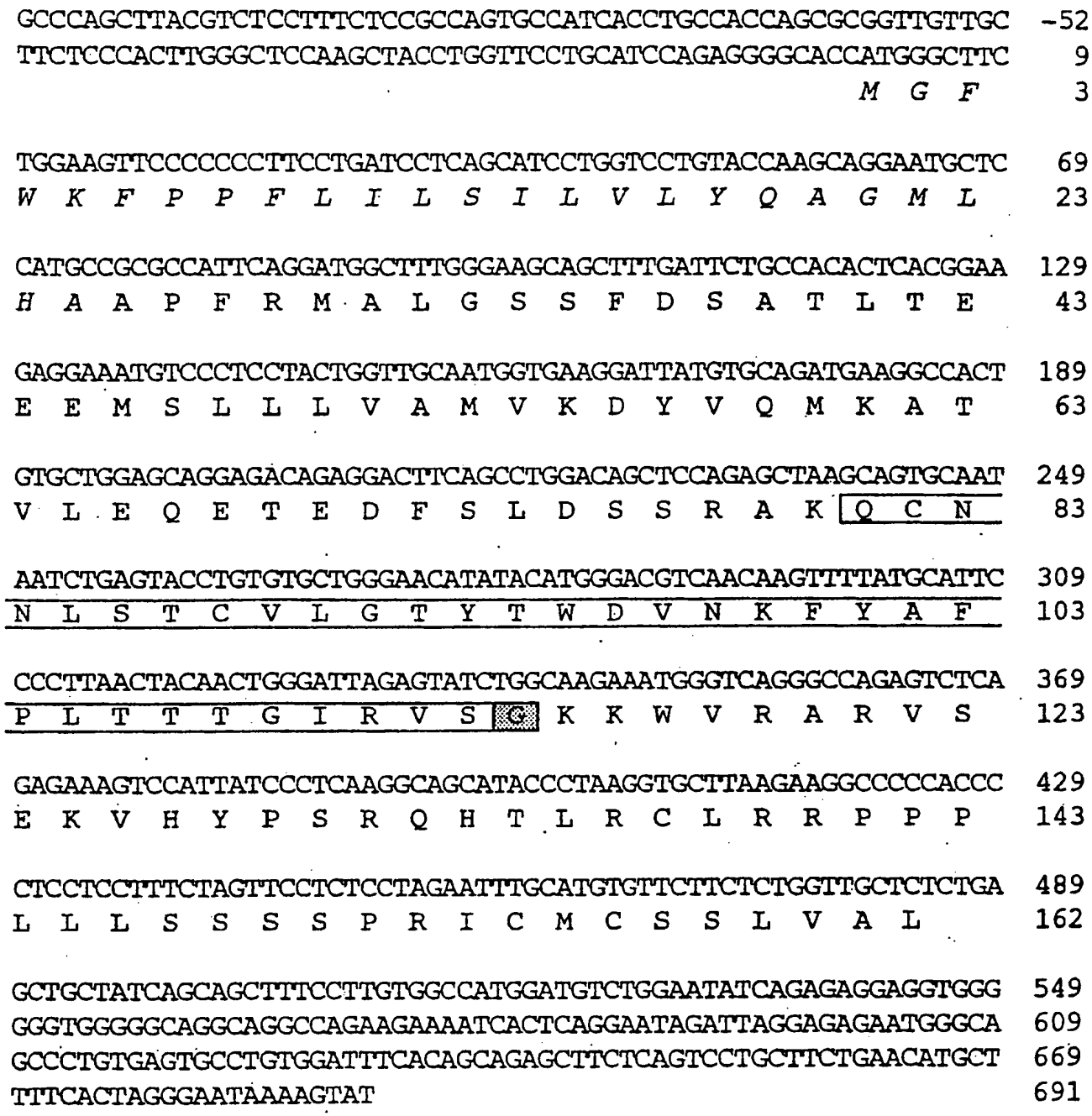
Fig. 22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P L T T T G I R V S Q K K W V R A R V S 123
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E K V H Y P S R Q H T L R C L R R P P P 143
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L L L S S S S P R I C M C S S L V A L 162
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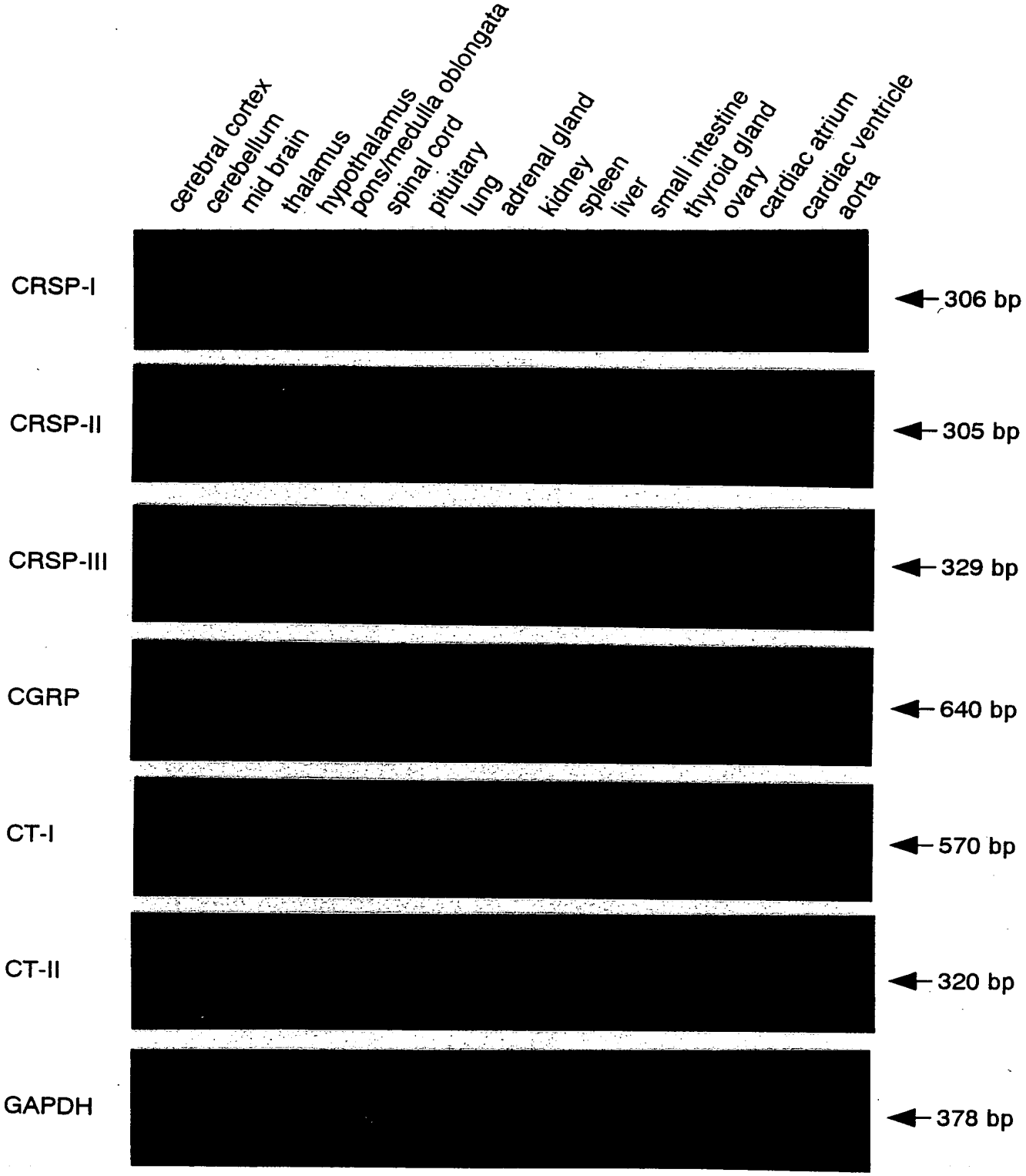
TTTCACTAGGGAATAAAAGTAT 691

Fig. 23

SCNTASCVTHKMTGWLSRSGSVAKNNFMP-TNVDSKIL-NH_2	pCRSP-2
SCNTAICVTHKMAGWLSRSGSVVKNNFMP-INMGSKVL-NH_2	pCRSP-3
SCNTATCMTHRLVGLLSRSGSMVRSNLLP-TKMGFKVFG-NH_2	pCRSP
SCNTATCVTHRLAGLLSRSGGMVKSNFVP-TDVGSEAF-NH_2	pCGRP
YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY-NH_2	pAM

CSNLSTCVLSAYWRNLNNFHRFSGMGFGPETP-NH_2	pCT
pECNNLSTCVLGTYTWDVNKFYAFPLTTTGIRVS-NH_2	pCT-2

Fig. 24


cerebral cortex
cerebellum
mid brain
thalamus
hypothalamus
pons/medulla oblongata
spinal cord
pituitary
lung
adrenal gland
kidney
spleen
liver
small intestine
thyroid gland
ovary
cardiac atrium
cardiac ventricle
aorta
CRSP-I
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CRSP-III
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CGRP
640 bp
CT-I
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CT-II
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GAPDH
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